Journal of the American Mosquito Control Association, 16(1):28–35, 2000

APPLICATION OF GEOGRAPHIC INFORMATION TECHNOLOGY IN DETERMINING RISK OF EASTERN EQUINE ENCEPHALOMYELITIS VIRUS TRANSMISSION

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ABSTRACT. Geographic information system (GIS) technology and remote sensing were used to identify landscape features determining risk of eastern equine encephalomyelitis virus (EEE) transmission as defined by the abundance of *Culiseta melanura* (the enzootic vector) and 6 putative epidemic–epizootic vectors in Massachusetts. Landsat Thematic Mapper data combined with aerial videography data were used to generate a map of landscape elements at epidemic–epizootic foci in southeastern Massachusetts. Geographic information system technology was used to determine the proportion of landscape elements surrounding 15 human and horse case sites where abundance data were collected for *Culiseta melanura, Aedes canadensis, Aedes vexans, Culex salinarius, Coquillettidia perturbans, Anopheles quadrimaculatus,* and *Anopheles punctipennis.* The relationships between vector abundance and landscape proportions were analyzed using stepwise linear regression. Stepwise regression indicated wetlands as the most important major class element, which accounted for up to 72.5% of the observed variation in the host-seeking populations of *Ae. canadensis, Ae. vexans,* and *Cs. melanura.* Moreover, stepwise linear regression demonstrated deciduous wetlands to be the specific wetland category contributing to the major class models. This approach of utilizing GIS technology and remote sensing in combination with street mapping can be employed to identify deciduous wetlands in neighborhoods at risk for EEE transmission and to plan more efficient schedules of pesticide applications targeting adults.

KEY WORDS Geographic information systems, eastern equine encephalomyelitis virus, remote sensing

INTRODUCTION

Recent studies have investigated the potential of a variety of mosquito species to serve as the epidemic vectors of eastern equine encephalomyelitis virus (EEE) in Massachusetts (Vaidyanathan et al. 1997; Moncayo and Edman, 1999). These potential vectors include (in order of relative importance) *Culex salinarius* (Coq.), *Aedes canadensis* (Theobald), *Coquillettidia perturbans* (Walker), *Anopheles quadrimaculatus* (Say), *Aedes vexans* (Meigen), and *Anopheles punctipennis* (Say). Controlling populations of these potential EEE vectors is of great interest to health officials, mosquito control workers, and the public at large. Identification of landscape elements that predispose humans and horses to risk of EEE transmission is important for understanding and controlling eastern equine encephalomyelitis. Landscape epidemiology or the ecological approach to the study of infectious agents was developed more than 50 years ago (Pavlovsky 1966, Fish 1996). In this study we adopted this approach because of the relationship that exists between the vectors that transmit EEE and the physical and biological features of the landscape. Features in the landscape such as vegetation provide food and other resources such as shelter and resting and developmental sites for mosquitoes. Geographic information system (GIS) technology allows the examination of remotely sensed landscape elements that relate to vector abundance, and therefore transmission risk. This technology has been used recently to answer epidemiologically relevant questions in a variety of arthropod-borne disease systems (Linthicum et al. 1990, Randolph 1993, Beck et al. 1994, Malone et al. 1994, Cross et al. 1996, Rogers et al. 1996, Dister et al. 1997, Gleiser and Gorla 1997, Thompson et al. 1997, Baylis et al. 1998, Estrada-Pena 1998, Hightower et al. 1998, Kitron 1998, Maloney et al. 1998, Omumbo et al. 1998, Wilson 1998).

In this study we have used GIS technology as a tool to study the landscape of epidemic foci of eastern equine encephalomyelitis in southeastern Massachusetts. The New England Gap Analysis Project (GAP) has developed base vegetation maps for New England by using Landsat Thematic Mapper (TM) (Space Imaging Inc., Thorton, CO) data (multispectral satellite data) combined with aerial videography (Slaymaker et al. 1996). The GAP was originally designed as a tool for determining the conservation status of components of biodiversity. The main purpose of the GAP has been to identify gaps (vegetation and animal species that are not represented in conservation areas) that may be filled through the creation of new reserves or improvement of land management. The GAP data provide many major forest, nonforest, wetland, urban, and water classifications that can be further separated into subtypes to obtain a more detailed perception of the landscape.

The New England landscape is 50–95% forested with a wide variety of forest types in relatively

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Table 1. Proportion of major landscape elements in the study area.

Landscape element	Area (m^2)	Proportion
Nonforest cover	15,379,452	0.33
Conifer	114,447,364	0.31
Wetlands	8,854,836	0.19
Fresh open water	3,262,308	0.07
Urban	2,330,220	0.05
Oak dominant	1,398,132	0.03
Oak–maple–birch	932,088	0.02
Red maple dominant	932,088	0.02
Total	46,604,400	1.00

small stands interspersed throughout the landscape. In southeastern Massachusetts, wetlands make up 20% of the land (Komar and Spielman 1994). Forested wetlands, some of which are now conservation areas, are important for a healthy water supply and flood protection for local residents. Wetlands also provide an important habitat for wildlife, including many species of birds and mosquitoes implicated in the EEE cycle. Residential development within or adjacent to forested wetland areas has brought an increasing number of humans and horses in contact with mosquitoes capable of transmitting EEE (Komar and Spielman 1994).

The GAP data were used to describe the landscape composition of 15 case sites resulting from the most recent major eastern equine encephalomyelitis epidemics in Massachusetts in the 1980s and 1990s. Our objective was to identify landscape elements that are highly correlated with population abundance of the enzootic vector of EEE, *Culiseta melanura* (Coq.), as well as with the potential epidemic vectors in Massachusetts.

MATERIALS AND METHODS

Study site: This study focused on the southeastern corner of Massachusetts and specifically on Bristol and Plymouth counties, where the majority of human and horse cases have occurred historically. In addition, these 2 counties have the greatest record of virus isolations from mosquito pools (Massachusetts Department of Public Health, State Laboratory, Boston).

First, we developed a map based on locations of horse and human cases as well as virus isolates. To create this coverage we used a U.S. Geological Survey (USGS) 1:25,000 datalayer that was registered to a universal transverse mercator (UTM) real-world coordinate system. This allows proper scaled orientation of case locations.

Landscape map generation: A major component of this study was the use of remotely sensed data that were already available in the New England GAP analysis homepage (Finn and Griffin 1999). Particular attention was made to landscape elements associated with mosquito abundance (e.g., palustrine wetlands). The accuracy of GAP classification data was verified by comparing Landsat TM classifications with ground cover examined by field mapping. These data were in ArcInfo (Environmental Systems Research Institute Inc., Redlands, CA) grid format (Raster data set; i.e., nonpolygon). Landscape elements identified by this data set include the following 11 major type categories: northern hardwoods, red maple dominant, oak dominant, birch dominant, oak–maple–birch codominant, conifer, maple–oak–conifer codominant, palustrine wetlands, nonforest cover, fresh open water, and urban elements. Each of these major types was further broken down into subtypes so that a more detailed landscape could be visualized. A total of 64 such subtype elements were available from this data set. Eight of the 11 major type categories were identified in our study area with only northern hardwoods, birch dominant, and maple–oak–conifer codominant missing.

Mosquito abundance data: Population abundance data were obtained through trapping performed from mid-July to mid-September, 1996. ABC traps (American Biophysics Corporation, East Greenwich, RI) traps were used to sample adult mosquito populations at 15 epidemic sites. Traps were equipped with 2 attractants: a photosensitive flickering light that responds to changes in light intensity and starts operating at dusk, and compressed CO_2, which was continuously emitted at 500 ml/min from a storage tank. This flow rate was intended to mimic the average CO_2 discharge from a medium- to large-sized mammal such as an adult human. Two ABC traps were placed at each case site during 2 consecutive nights each week. The average seasonal population abundances obtained for each of the 6 putative EEE epidemic vectors (*Ae. canadensis, Ae. vexans, Cq. perturbans, Cx. salinarius, An. quadrimaculatus,* and *An. punctipennis*) and the known enzootic vector (*Cs. melanura*) were used to construct our linear regression models.

Landscape–mosquito abundance analysis: We projected existing USGS case site coverages into the GAP data coordinate system (UTM zone 19 to UTM zone 18). Each of the 15 case sites was buffered (delineated) around an area 1 km in radius from the case site (Fig. 1). This 1-km distance was an arbitrary distance based on an average flight range for mosquitoes (Hobbs et al. 1974). The buffered areas were clipped out and converted to polygons. The polygonal buffers were overlaid on the landscape map to calculate the proportion of the area that each landscape element occupied within the buffer. We calculated the area of each landscape category in acres for each buffered area.

Before variable selection through stepwise linear regression, linear regression models of the nontransformed data were created. The Y and $\log(Y)$ were fitted in the proportions $p1, \ldots, p(c-1)$, where p values are untransformed major class landscape element proportions, Y is the average mosquito abundance per trap night during the summer of 1996, and

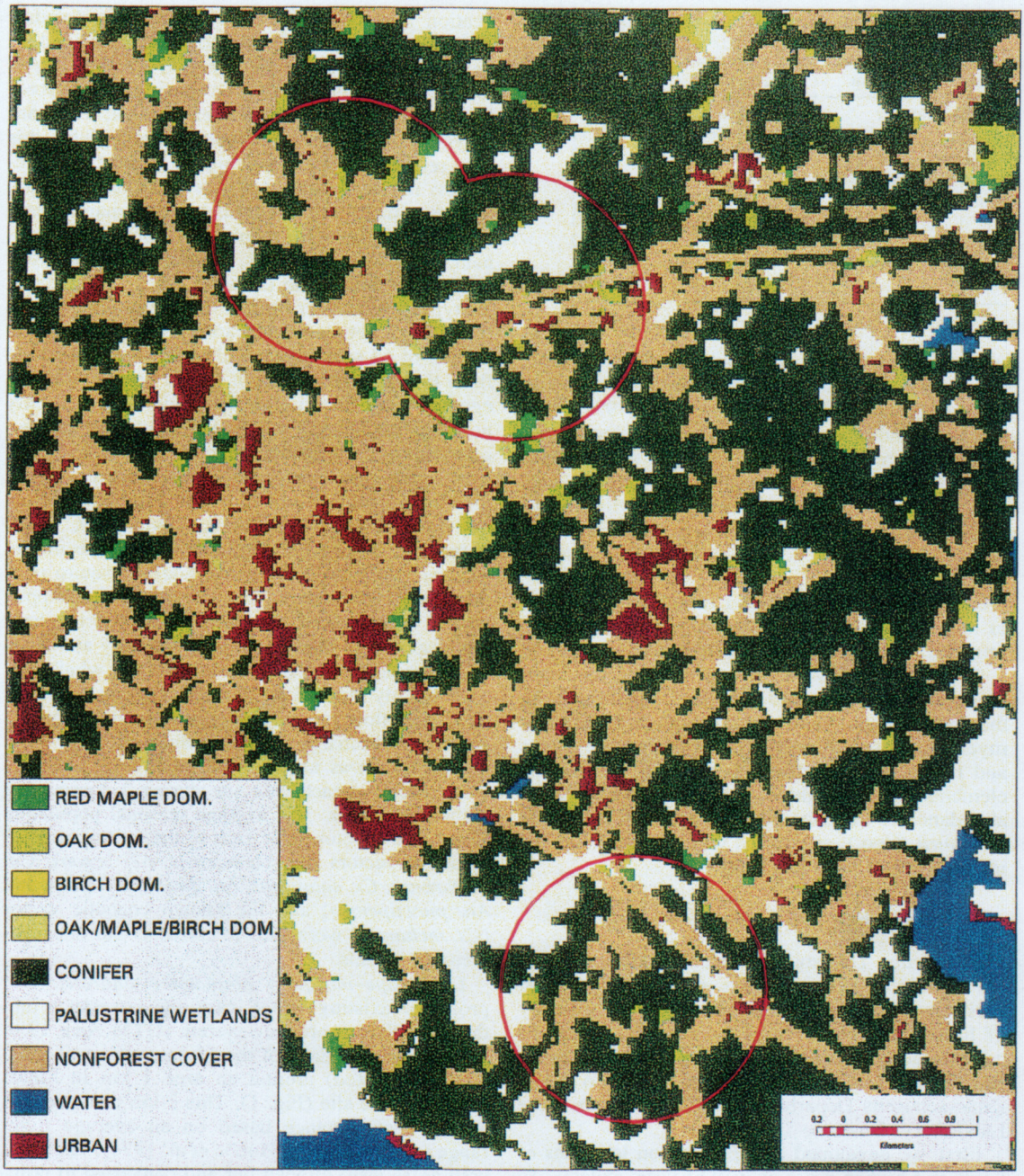

Fig. 1. Subset of buffered case sites in study area (data from National Gap Analysis Project).

c is the total number of major landscape elements. After this, the residuals were plotted versus the fitted value Y and $\log(Y)$ and each of the proportions, to examine assumptions of linearity and constant variance.

The assumptions of linearity and constant variance were better conserved when the log-transformed population data were used for *Ae. canadensis, Cx. salinarius,* and *Ae. vexans.* Transformed abundance data were therefore used in building the stepwise linear regression models with untransformed proportions.

Stepwise linear regressions were constructed to identify the best set of landscape proportions for predicting abundance of each of the 6 species. These sets were then used to develop linear models. The log-transformed mosquito average abundances were used as the dependent variables and the proportions

Table 2. Proportion of major landscape categories within 1-km radius from each trap site in each town.

Town	Area (m^2)	Red maple dominant	Oak dominant	Oak–maple–birch	Conifer dominant	Wetland	Nonforest cover	Water	Urban	Total
Norton	3,125,700	0.00	0.02	0.01	0.26	0.22	0.25	0.16	0.08	1.00
Middleboro–NW	3,087,000	0.01	0.03	0.01	0.40	0.16	0.38	0.00	0.01	1.00
Middleboro–NE	3,131,100	0.02	0.04	0.02	0.45	0.22	0.24	0.00	0.02	1.01
Middleboro–S	3,123,000	0.00	0.01	0.00	0.51	0.16	0.31	0.00	0.01	1.00
Lakeville	3,126,600	0.02	0.03	0.01	0.29	0.08	0.19	0.38	0.00	1.00
Rochester	3,121,200	0.01	0.04	0.01	0.54	0.19	0.21	0.00	0.01	1.01
Onset	3,000,000	0.00	0.01	0.01	0.35	0.04	0.22	0.25	0.17	1.05
Wareham	3,000,000	0.00	0.00	0.00	0.49	0.03	0.19	0.24	0.02	0.97
Kingston–S	3,130,200	0.01	0.02	0.00	0.40	0.17	0.35	0.00	0.04	0.99
Kingston–N	3,127,500	0.00	0.02	0.00	0.32	0.33	0.23	0.01	0.09	1.00
Pembroke	3,126,600	0.00	0.01	0.00	0.32	0.07	0.53	0.03	0.04	1.00
Abington	3,126,600	0.06	0.09	0.01	0.16	0.16	0.48	0.00	0.04	1.00
Whitman	3,128,400	0.06	0.10	0.08	0.08	0.11	0.53	0.00	0.04	1.00
Brockton	3,123,900	0.04	0.06	0.06	0.02	0.06	0.68	0.00	0.10	1.02
Bridgewater	3,126,600	0.00	0.01	0.05	0.01	0.80	0.11	0.00	0.01	0.99

of landscape variables were used as the independent variables. Landscape proportions were thus added to the equations for each of the 6 species until none of the remaining variables improved the model.

The 1st regression models for the 6 species used the major landscape categories available in the GAP data set. Table 1 shows the distribution of major landscape classes in the entire study area. Table 2 is a list of the proportions of the major landscape categories within a 1-km radius from each trap site in each town surveyed.

Once a determination was made of which major type categories were good predictors of species abundance, we performed another set of stepwise linear regressions to tease out the major type subclasses that most contribute to the major class models for each species.

RESULTS

Landscape description

The study area (combined buffered areas around each trap site) was found to be composed of 8 different major landscape classes as defined by the GAP data set (Table 1). The predominant landscape feature was nonforest cover (33%). This was followed by 31% conifer, 19% wetlands, 7% fresh open water, 5% urban, 3% oak dominant, 2% oak–maple–birch mixture, and 2% red maple dominant.

The proportion that each landscape element contributes to the total study area (Table 1) does not necessarily follow the order of the contribution of each landscape element in a particular town (Table 2). For example, in Bridgewater, the element that most contributes to the area 1 km around the trap site is not nonforest cover, as would be expected by looking at the combined landscape buffer zones, but rather wetlands (80%).

Stepwise linear regressions with major class predictors of mosquito abundance

We found that wetlands accounted for 72.5% of the observed variation in abundance of *Ae. canadensis* populations (Table 3). This association was positive (Fig. 2). The conifer-dominant element accounted for 12.5% of the variation observed in the population abundance of this same species. The conifer-dominant landscape proportion was positively associated with abundance of *Ae. canadensis* but was not highly correlated with it ($r = 0.071$; Table 3 and Fig. 3). The regression analysis of variance showed the equation log(mosquito average abundance) = 0.188 + (2.598 × wetland proportion) + (6.716 × conifer-dominant proportion) to be a good predictor of abundance of *Ae. canadensis* during the summer season (F ratio = 10.094, $P = 0.000$).

Conifer dominant was the landscape element that contributed most to the *Ae. vexans* major class model, accounting for 52.5% of the observed var-

Table 3. Results of stepwise linear regression based on major type landscape categories.

Species	Variable	R	R^2	SEE[1]	F ratio	P
Aedes canadensis	Wetland	0.851	0.725	0.2959	34.221	0.000
	Wetland + conifer	0.922	0.850	0.2270	10.094	0.000
Aedes vexans	Conifer	0.725	0.525	0.2801	14.379	0.002
	Conifer + wetland	0.836	0.700	0.2319	6.966	0.001
Culiseta melanura	Wetland	0.694	0.482	0.1991	12.108	0.004

[1]SEE, standard error of the estimate.

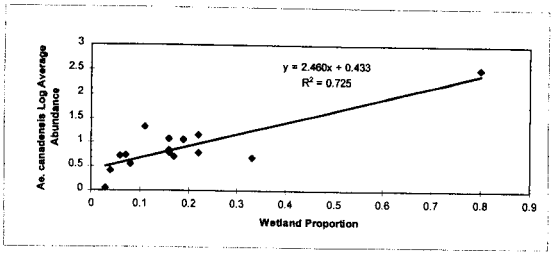

Fig. 2. Linear regression of *Aedes canadensis* log average abundance and wetland proportion.

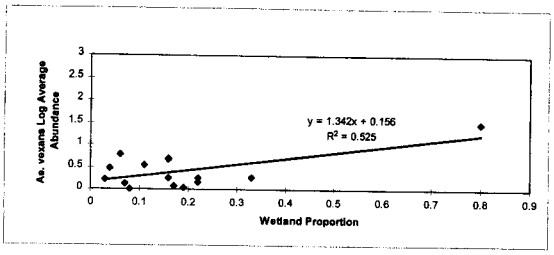

Fig. 4. Linear regression of *Aedes vexans* log average abundance and wetland proportion.

iation in mosquito abundance (Table 3). The conifer element was negatively correlated with mosquito abundance (Fig. 5). When wetland was added to this model, the R^2 value increased from 0.525 to 0.700, which translates to an r value increase (a better measure of the correlation between mosquito abundance and landscape variables) from 0.725 to 0.836. The standard error of the estimate, which estimates the standard deviation around the regression line, was decreased from 0.2801 to 0.2319 with the addition of the wetland category. The wetlands element was positively correlated with abundance (Fig. 4). The equation log(mosquito average abundance) = 0.625 + (−1.283 × conifer-dominant proportion) + (0.925 × wetland proportion) was a good predictor of abundance of *Ae. vexans* during the summer season (F ratio = 6.966, P = 0.001).

Wetlands was the major class element that accounted for most of the variation seen in the abundance of *Cs. melanura* populations (R^2 = 0.482). Again, wetlands were positively correlated with log average abundance of this species (r = 0.694; Table 3 and Fig. 6). The equation log(mosquito average abundance) = 0.324 + (0.978 + wetland proportion) was an adequate predictor of abundance (F ratio = 12.108, P = 0.004). Stepwise linear regression with major types was not able to devise a model that would predict the abundance of *Cq. perturbans, Cx. salinarius, An. quadrimaculatus,* or *An. punctipennis.*

Stepwise linear regressions with subclass predictors of mosquito abundance

Stepwise linear regressions were then performed to tease out the wetland subclasses that most contributed to the major class models. In all cases, deciduous wetland was the specific wetland category that contributed most to the models that relate landscape elements to abundance of the populations of *Ae. canadensis, Ae. vexans, Cx. salinarius,* and *Cs. melanura* (Table 4 and Figs. 7–10). Deciduous wetlands best accounted for the observed variation in populations of *Ae. canadensis* (R^2 = 0.834), followed by *Cs. melanura* (R^2 = 0.527), *Ae. vexans* (R^2 = 0.442), and *Cx. salinarius* (R^2 = 0.317). The regression equations for predicting mosquito abundance were as follows: for *Ae. canadensis*: log(mosquito average abundance) = −0.0137 + (1.611 × deciduous wetland proportion) + (2.827 × scrub or shrub marsh proportion) + (1.944 × emergent persistent proportion) (F ratio = 5.067, P = 0.000); for *Cs. melanura*: log(mosquito average abundance) = 0.264 + (0.894 × deciduous wetland proportion) (F ratio = 14.498, P = 0.002); for *Ae. vexans*: log(mosquito average abundance) = 0.292 + (1.091 × deciduous wetland proportion) + (−3.028 × mixed deciduous conifer wetland proportion) (F ratio = 8.113, P = 0.001); for *Cx. salinarius*: log(mosquito average abundance) = 0.215 + (1.531 × deciduous wetland proportion) (F ratio = 6.043, P = 0.029). Construction of stepwise linear regression models was not possible for the wetland subclasses for *Cq. perturbans* or the *Anopheles* species.

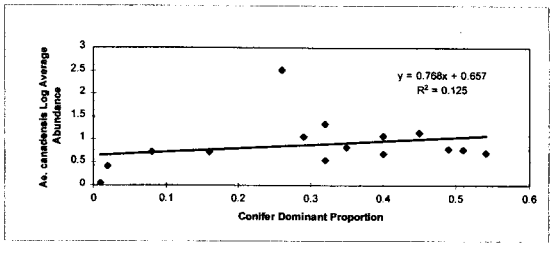

Fig. 3. Linear regression of *Aedes canadensis* log average abundance and conifer dominant proportion.

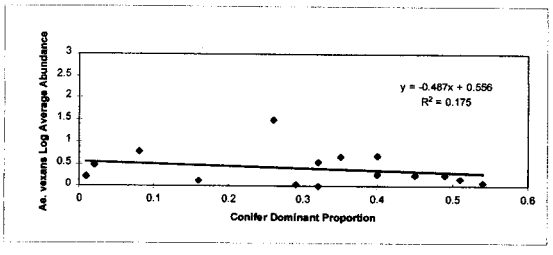

Fig. 5. Linear regression of *Aedes vexans* log average abundance and conifer dominant proportion.

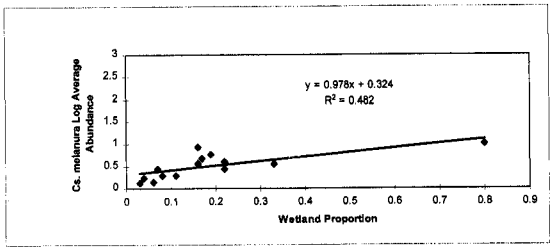

Fig. 6. Linear regression of *Culiseta melanura* log average abundance and wetland proportion.

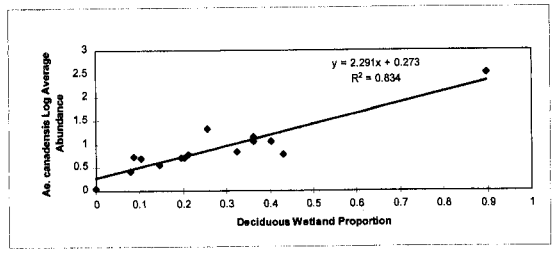

Fig. 7. Linear regression of *Aedes canadensis* log average abundance and deciduous wetland proportion.

DISCUSSION

The aim of this study was to use remotely sensed landscape information to determine environmental elements that predispose humans and horses to EEE transmission. In Massachusetts, Atlantic white cedar (*Chamaecyparis thyoides*) and red maple (*Acer rubrum*) swamps provide optimal habitat for the development of larvae of *Cs. melanura.* Adult *Cs. melanura* are found in large numbers in light traps set near these forested wetlands. This species is responsible for the maintenance and amplification of EEE in reservoir birds throughout the United States (Edman et al. 1993). Reservoir hosts, for example, American robins (*Turdus migratorius*) and red-winged blackbirds (*Agelaius quiscula*), are known to form roosts in forested swamps (Komar and Spielman 1994). In order for a bridge or epidemic–epizootic vector to obtain EEE, the vector must take a blood meal from the reservoir host. This infective epidemic–epizootic vector can then transmit the virus by taking a subsequent blood meal from a naive mammalian host. Although occupying different niches, the 6 potential vectors of EEE in Massachusetts have been obtained from light traps at epidemic foci near forested wetlands. The focus of this study was to identify the type of habitat that contributes to the appearance and population size of *Cx. salinarius, Ae. canadensis, Cq. perturbans, An. quadrimaculatus, Ae. vexans,* and *An. punctipennis.* Because the population data used for this analysis were obtained from CO_2-baited ABC light traps, the data represent 60–70% of the proportion of the population attracted to a human host during a 2-h period beginning at sunset (Vaidyanathan and Edman 1997). The habitats identified in this study represent habitats that best correlate with trapped adult populations.

Wetlands were found to account for 72.5% of the observed variation in the abundance of *Ae. canadensis* populations and 48.2% of the variation in *Cs. melanura* populations. More specifically, the deciduous (or leafy) wetlands accounted for the variation seen in populations of these 2 species (83.4 and 52.7%, respectively). This is consistent with the known biology of these 2 mosquito species. Wooded swamps and adjacent hardwood forests are the main types of habitats for both larval and adult *Cs. melanura* (Joseph and Bickley 1969). *Aedes canadensis* develop in temporary woodland pools containing decaying leaves. These sites have been documented as being closely associated with swamp habitats of *Cs. melanura* (Carpenter et al. 1946, Main et al. 1968). In addition, female *Ae. canadensis* remain close to the forest margin even when host seeking at dusk and in the early evening (Hayes 1962, Trueman and McIver 1986).

Conifer dominant accounted for 52.5% of the observed variation of *Ae. vexans* populations and was 72.5% correlated (F ratio = 14.379, $P = 0.002$) with these populations. However, this variation was negatively correlated with this landscape type. *Aedes vexans* develops in open meadows or grassy depressions and river and stream floodplains (Carpenter et al. 1946, Horsfall et al. 1973, Komar and Spielman 1994). Conifer-dominant areas do not provide the type of floodwater habitat that promotes

Table 4. Results of stepwise linear regression based on wetland subcategories.

Species	Variable	*R*	R^2	SEE	F ratio	*P*
Aedes canadensis	Deciduous wetland	0.913	0.834	0.2295	65.499	0.000
	Deciduous wetland + scrub or shrub marsh	0.945	0.894	0.1911	6.740	0.000
	Deciduous wetland + scrub or shrub marsh + emergent persistent	0.963	0.927	0.1652	5.067	0.000
Aedes vexans	Deciduous wetland	0.665	0.442	0.3036	10.313	0.007
	Deciduous wetland + mixed Deciduous–Conifer	0.817	0.667	0.2441	8.113	0.001
Culex salinarius	Deciduous wetland	0.563	0.317	0.5048	6.043	0.029
Culiseta melanura	Deciduous wetland	0.726	0.527	0.1903	14.498	0.002

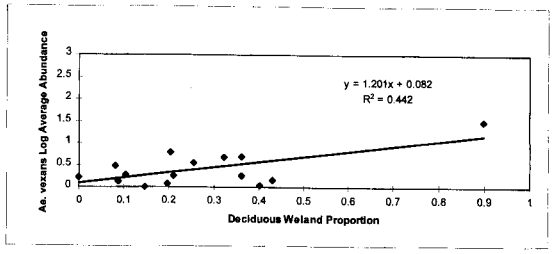

Fig. 8. Linear regression of *Aedes vexans* log average abundance and deciduous wetland proportion.

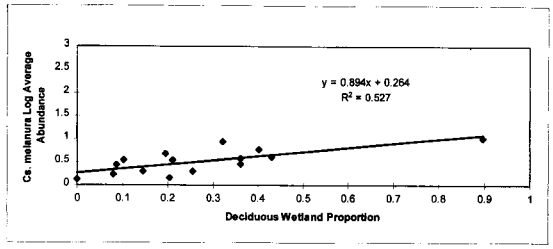

Fig. 10. Linear regression of *Culiseta melanura* log average abundance and deciduous wetland proportion.

the presence of *Ae. vexans*. This species was correlated with wetlands and more specifically deciduous wetlands (r = 0.665). Adults of this species rest in damp woods.

Derivaton of a major class model was not possible for *Cx. salinarius, Cq. perturbans,* and the 2 *Anopheles* species. However, we were able to detect a correlation between deciduous wetlands and variation in population sizes of *Cx. salinarius.*

We have identified deciduous wetlands as the specific landscape category that contributes most to the abundance of *Cs. melanura, Ae. canadensis, Ae. vexans,* and *Cx. salinarius* and, therefore, risk of EEE transmission. Therefore, targeting of deciduous wetlands by mosquito control practitioners can reduce populations of enzootic and several potential epidemic vectors of EEE. Landscape maps derived from GAP data can be combined with street address data to better plan pesticide applications. Although a stepwise linear regression did not correlate *Cq. perturbans* abundances with any specific landscape feature, their larval habitats are well known. Larvae puncture roots of emergent vegetation (cattail, water lettuce, swamp loosestrife, arrow arum, and maidencane) in permanent freshwater marshes (Crans and Schulze 1986, Morris et al. 1990). Emergent persistent vegetation is a distinguishable subcategory of the wetlands GAP data classification and, therefore, can also be mapped based on these TM data to help direct planning strategies against this potentially important EEE vector.

ACKNOWLEDGMENTS

We thank the Office of Geographic Information Analysis at the University of Massachusetts for the use of their personnel and facilities. Special thanks to Meghan S. Moncayo for assistance in obtaining mosquito abundance data used in this study. This study was funded by a grant from the Massachusetts Department of Public Health and from Hatch support from the Massachusetts Agricultural Experiment Station.

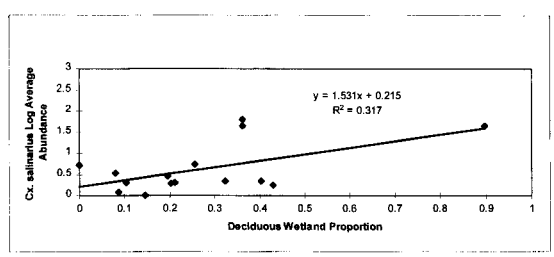

Fig. 9. Linear regression of *Culex salinarius* log average abundance and deciduous wetland proportion.

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